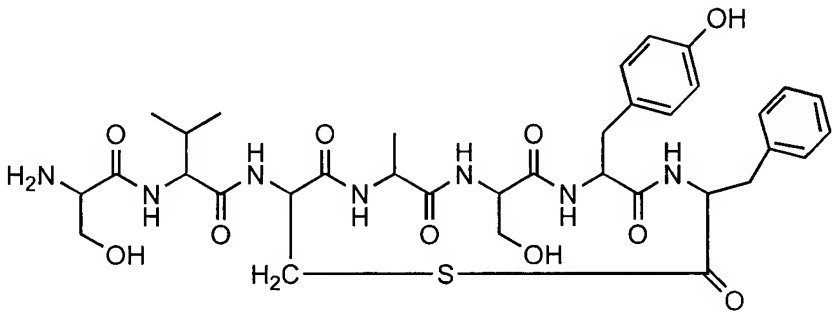
Amendments to the Specification:

Please replace paragraph [0049] on page 11 with the following rewritten paragraph:

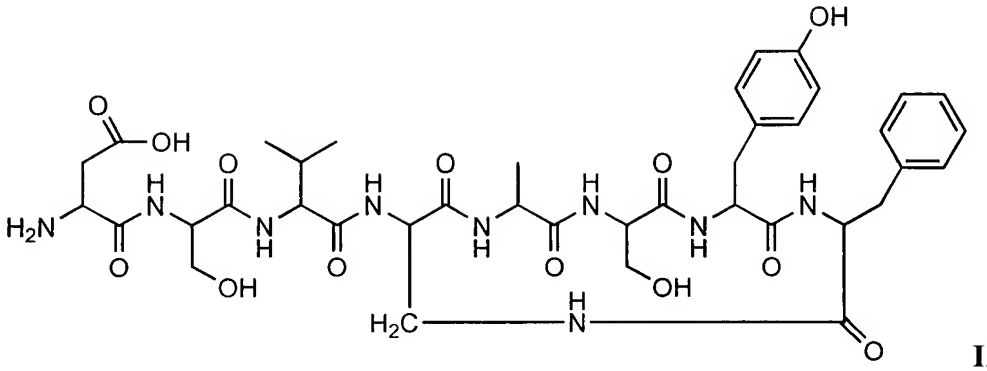
[0049] Figure 12 shows the alignment of LuxS and YgaG protein sequences. The translated protein sequences for the AI-2 production family of proteins are shown. We determined the sequences for the *luxS*$_{V.h.}$ gene from *V. harveyi* BB120 (SEQ ID NO: 10), and the *ygaG* genes (re-named herein as *luxS*$_{E.c.}$ from *E. coli* MG1655 (SEQ ID NO: ~~25~~ 26), *E. coli* O157:H7 (SEQ ID NO: 11), and *E. coli* DH5α (SEQ ID NO: ~~26~~ 27). The *S. typhimurium* LT2 *ygaG* (SEQ ID NO: 36) (re-named herein *luxS*$_{S.t.}$ partial sequence came from the *S. typhimurium* database. Amino acid residues that are not identical to the LuxS$_{V.h.}$ protein are underlined and not in bold font. The site of the frame shift mutation in the *E. coli* DH5α DNA sequence is denoted by an "*." The 20 altered amino acid residues that are translated following the frame shift are enclosed by the box.

Please replace paragraph [0193] on page 42 with the following rewritten paragraph:

[0193] Examples of inhibitors of peptide-mediated quorum sensing molecules include chemically-modified pheromones of *Staphylococcus epidermidis* that are competent inhibitors of the *Staphylococcus aureus* agr (accessory gene regulator) system. These inhibitors include molecules of the structures VIII and IX:



VIII



IX

(*cyclo*-SVCASYF) (SEQ ID NO: 28)

(*cyclo*-DSV(DAPA)ASYF) (SEQ ID NO: 29)

Please replace paragraph [0195] on page 42 with the following rewritten paragraph:

[0195] Further inhibitors of peptide-mediated quorum sensing are compounds of the structure:

(cyclo)-YSTCDFIM;(X) (SEQ ID NO: 30)

(cyclo)-GVNACSSLF;(XI) (SEQ ID NO: 31)

(cyclo)-GVNASSSLF; or(XII) (SEQ ID NO: 32)

(cyclo)-GVNA(DAPA)SSLF, (XIII) (SEQ ID NO: 33)

wherein in these four structures the C-terminal carbonyl group forms 1) a thiolactone with the sulfur atom of the cysteine residue (YSTCDFIM (SEQ ID NO: 30) and GVNACSSLF (SEQ ID NO: 31)); 2) a lactone group with the oxygen atom of the first serine residue (GVNASSSLF) (SEQ ID NO: 32); or 3) an amide bond with amino group of the diaminoproprionic acid (DAPA) residue (GVNA(DAPA)SSLF) (SEQ ID NO: 33). The synthesis of these molecules and activity of these molecules have been described in Mayville et al., Proc. Natl. Acad. Sci. USA, 96, 1218-1223 (1999).

Please replace paragraph [0275] on page 70 with the following rewritten paragraph:

[0275] Analysis of the AI-2 Production Genes from *V. harveyi*, *E. coli* and *S. typhimurium*. We sequenced the AI-2 production gene $LuxS_{V.h.}$ from *V. harveyi* BB120 and the *ygaG* loci from *E. coli* O157:H7, *E. coli* MG1655 and *E. coli* DH5α. The translated protein sequences encoded by the *ygaG* ORF's are shown in Figure 12, and they are aligned with the translated LuxS protein sequence from *V. harveyi*. The non-bold, underlined amino acids indicate the residues in the *E. coli* proteins that differ from the *V. harveyi* LuxS protein. The *ygaG* loci from *E. coli* encode proteins that are highly homologous to one another and also to LuxS from *V. harveyi*. The *E. coli* MG1655 (SEQ ID NO: ~~25~~ 26) and the *E. coli* O157:H7 (SEQ ID NO: 11) YgaG proteins are 77% and 76% identical to LuxS from *V. harveyi* BB120 (SEQ ID NO: 10). The DNA sequence we determined for *ygaG* from *E. coli* O157:H7 differs at five sites from the reported (and our) sequence for the *E. coli* MG1655 *ygaG* gene. Four of the changes are silent, the fifth results in a conservative Ala to Val alteration at amino acid residue 103 in the *E. coli* O157:H7 protein.

Please replace paragraph [0298] on page 79 with the following rewritten paragraph:

[0298] Crude peptides are isolated on a Waters 600 Multi Solvent Delivery System equipped with a Lambda Max Model 481 as detector. A semi-preparative column (Nucleosil C18, 4x250mm; 5 m; Grom, Herrenberg, Germany) is eluted at a flow rate of 3.5 ml/min with a linear gradient (10-100% B in A in 45 min; solvent A: 0.1% trifluoroacetic acid (TFA) in water; solvent B: 0.1% TFA in acetonitrile). The detection wavelength is 214 nm. The concentration of purified peptides, redissolved in dimethylsulfoxide (DMSO), is determined using analytical HPLC on a Kontron HPLC System with Kroma System 2000 software. An analytical column (Spherisorb ODS2 2x100 mm; 5 μM; Grom, Herrenberg, Germany) is eluted at a flow rate of 250 μl/min with a linear gradient (0-100% B in A in 30 min; solvent A: 0.1 % TFA in water; solvent B: 0.1% TFA in acetonitrile). The detection wavelength is 214 nm. A known amount of the (unmodified) peptide DSVCASYF (SEQ ID NO: 34) is used as a reference. The amount of delta-toxin is quantified using the same system. A Pharmacia Resource PHE 1 ml column is

eluted with 1.5 column volumes of a linear gradient (0-100% of B in A; A: 0.1% TFA in water; B: 0.1% TFA in acetonitrile). The S. epidermidis delta-toxin is eluted using the same conditions on a ÄKTA explorer 100 system (Amersham Pharmacia Biotech, Freiburg, Germany). The isolated delta-toxin is chemically analyzed by ESI-MS.

Please replace paragraph [0305] on page 82 with the following rewritten paragraph:

[0305] Cyclic peptides of the formula (cyclo)-YSTCDFIM (SEQ ID NO: 30); (cyclo)-GVNACSSLF (SEQ ID NO: 31); (cyclo)-GVNASSSLF (SEQ ID NO: 32); and (cyclo)-GVNA(DAPA)SSLF (SEQ ID NO: 33), in which the C-terminal carbonyl group forms a thiolactone with the sulfur atom of the cysteine residue (YSTCDFIM (SEQ ID NO: 30) and GVNACSSLF (SEQ ID NO: 31)); a lactone group with the oxygen atom of the first serine residue (GVNASSSLF) (SEQ ID NO: 32); or an amide bond with amino group of the diaminoproprionic acid (DAPA) residue (GVNA(DAPA)SSLF (SEQ ID NO: 33); are synthesized through use of the Fmoc/tBu strategy on Tritylresin (PepChem: Clausen and Goldammer, Tübingen, Germany). The sequence of the peptide is DSVXASYF (SEQ ID NO: 35), with cysteine (C), serine (S) or 1,3-diaminopropionic acid (Dpr) in the X position. The corresponding protected amino acids for the synthesis of cyclic peptides are Fmoc-Cys(Mmt)-OH, Fmoc-Ser(Trt)-OH (both cleavable with TFA:TIS in dichloromethane) and Fmoc-Dpr(Dde)-OH (cleavable with hydrazine). The cyclic peptides are synthesized and purified according to M Otto, et al. (1998) FEBS Lett. 424, 89-94. The purity of peptides (> 90%) is controlled by RP-C18 chromatography and ESI-MS.

Please replace paragraph [0335] on page 95 with the following rewritten paragraph:

[0335] Analysis of the Effect of Autoinducer on SdiA Regulated Gene Expression. A sequence that includes the *ftsQ1p* and *ftsQ2p* promoters (Wang *et al.*, 1991, *supra*) was amplified from *E. coli* MG1655 chromosomal DNA using the following primers: *ftsQ1p*, 5'-CGGAGATCTGCGCTTTCAATGGATAAACTACG-3' (SEQ ID NO: 18); *ftsQ2p*, 5'-CGCGGATCCTCTTCTTCGCTGTTTCGCGTG-3' (SEQ ID NO: 19). The amplified product contained both the *ftsQ* promoters and the first 14 codons of the *ftsQ* gene flanked by *Bam*HI and

*Bgl*II sites. The *ftsQ1p2p* PCR product was cloned into the *Bam*HI site of vector pMLB1034 (Silhavy *et al.*, Experiments with Gene Fusions, Cold Spring Harbor Press, 1984) to generate a *lacZ* fusion that contained the promoters, ribosome-binding site, and initiation codon of *ftsQ*. A correctly oriented clone, pMS207, and a clone containing the *ftsQ1p2p* insert in the opposite orientation, pMS209, were chosen for further analysis. Both inserts were sequenced to ensure that no errors were introduced during the PCR reaction.

Please replace paragraph [0343] on page 99 with the following rewritten paragraph:

[0343] Mutagenesis and Analysis of the AI-2 Production Gene in *S. typhimurium* LT2. MudJ insertion mutants of *S. typhimurium* LT2 were generated using a phage P22 delivery system as described (Maloy, S.R., Stewart, V.J., and Taylor, R.K. (1996) *Genetic analysis of pathogenic bacteria: a laboratory manual.* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.). Following growth to mid-exponential phase in LB containing 0.5% glucose, the *S. typhimurium* insertion mutants were tested for AI-2 production using the *V. harveyi* BB170 bioassay. The site of the MudJ insertion that inactivated the AI-2 production function in *S. typhimurium* was identified by PCR amplification and sequencing of the chromosomal DNA at the insertion junction. A two-step amplification procedure was used (Caetano-Annoles, G. (1993) *Meth. Appl.* 3, 85-92). In the first PCR reaction, the arbitrary primer 5'-GGCCACGCGTCGACTAGTACNNNNNNNNNNACGCCC-3' (SEQ ID NO: 20), and the MudJ specific primer 5'-GCACTACAGGCTTGCAAGCCC-3' (SEQ ID NO: 21) were used. Next, 1 µl of this PCR reaction was used as the template in a second PCR amplification employing a second arbitrary primer (5'-GGCCACGCGTCGACTAGTCA-3') (SEQ ID NO: 22) and another MudJ specific primer (5'-TCTAATCCCATCAGATCCCG-3') (SEQ ID NO: 23). The PCR product from the second reaction was purified and sequenced.

Please replace paragraph [0344] on page 99 with the following rewritten paragraph:

[0344] Cloning and Sequencing of the *E. coli* MG1655, *E. coli* O157:H7, and *E. coli* DH5α AI-2 Production Genes. The DNA sequence obtained from the *S. typhimurium* LT2

MudJ screen was used to search the *E. coli* MG1655 genome sequence to identify the corresponding *E. coli* region (Blattner *et al.*, Science 277, 1453-1462, 1997). The gene identified from the sequencing project had the designation *ygaG*. Primers that flanked the *ygaG* gene and incorporated restriction sites were designed and used to amplify the *E. coli* MG1655, *E. coli* O157:H7 and *E. coli* DH5α *ygaG* genes. The primers used are: 5'-GTGAAGCTTGTTTACTGACTAGATC-3' (SEQ ID NO: 24) and 5'-GTGTCTAGAAAAACACGCCTGACAG-3' (SEQ ID NO: 25). The PCR products were purified, digested, and cloned into pUC19. In each case, the PCR products from three independent reactions were cloned and sequenced.